

RAW SEQUENCE LISTING

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Application Serial Number: 10/802,332A
Source: 1F4/6
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RAW SEQUENCE LISTING

DATE: 03/07/2006

PATENT APPLICATION: US/10/802,332A

TIME: 10:59:48

Input Set : A:\14875-040003.txt

Output Set: N:\CRF4\03072006\J802332A.raw

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3 <110> APPLICANT: KIMURA, NAOKI
4      TOYOSHIMA, TOMOKO
6 <120> TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
8 <130> FILE REFERENCE: 14875-040003
10 <140> CURRENT APPLICATION NUMBER: 10/802,332A
11 <141> CURRENT FILING DATE: 2004-03-16
13 <150> PRIOR APPLICATION NUMBER: US 09/855,266
14 <151> PRIOR FILING DATE: 2001-05-14
16 <150> PRIOR APPLICATION NUMBER: US 09/411,722
17 <151> PRIOR FILING DATE: 1999-10-01
19 <150> PRIOR APPLICATION NUMBER: PCT/JP98/01511
20 <151> PRIOR FILING DATE: 1998-04-01
22 <150> PRIOR APPLICATION NUMBER: JP 9/099653
23 <151> PRIOR FILING DATE: 1997-04-01
25 <160> NUMBER OF SEQ ID NOS: 14
27 <170> SOFTWARE: PatentIn version 3.3
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 176
31 <212> TYPE: PRT
32 <213> ORGANISM: Mus musculus
34 <400> SEQUENCE: 1
35 Met Val Thr Phe Ser His Val Ser Ser Leu Ser His Trp Phe Leu Leu
36 1          5          10          15
38 Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe Ala Met Pro Glu
39          20          25          30
41 Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln Ser Asn Asp Val
42          35          40          45
44 Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys Ala Pro Cys Lys
45          50          55          60
47 Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe
48 65          70          75          80
50 Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu Cys Ser Thr Cys
51          85          90          95
53 Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg
54          100         105         110
56 Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro
57          115         120         125
59 Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu
60          130         135         140
62 Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser
63 145         150         155         160
65 Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile Val Phe Cys Ile
66          165         170         175

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69 <210> SEQ ID NO: 2
70 <211> LENGTH: 148
71 <212> TYPE: PRT
72 <213> ORGANISM: Mus musculus
74 <400> SEQUENCE: 2
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76 1 5 10 15
78 Ser Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys
79 20 25 30
81 Ala Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His
82 35 40 45
84 Pro Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu
85 50 55 60
87 Cys Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala
88 65 70 75 80
90 Thr Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp
91 85 90 95
93 Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly
94 100 105 110
96 Ile Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser
97 115 120 125
99 Ser Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile
100 130 135 140
102 Val Phe Cys Ile
103 145
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 1509
108 <212> TYPE: DNA
109 <213> ORGANISM: Mus musculus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (12)..(539)
115 <400> SEQUENCE: 3
116 agctcacagc c atg gtt acc ttc agc cac gtc tcc agt ctg agt cac tgg 50
117 Met Val Thr Phe Ser His Val Ser Ser Leu Ser His Trp
118 1 5 10
120 ttc ctc ttg ctg ctg ctg ctg aat ctg ttc ttg ccg gta ata ttt gct 98
121 Phe Leu Leu Leu Leu Leu Leu Asn Leu Phe Leu Pro Val Ile Phe Ala
122 15 20 25
124 atg cct gaa tca tac tcc ttc aac tgt ccc gat ggt gaa tac cag tct 146
125 Met Pro Glu Ser Tyr Ser Phe Asn Cys Pro Asp Gly Glu Tyr Gln Ser
126 30 35 40 45
128 aat gat gtc tgt tgc aag acc tgt ccc tca ggt aca ttt gtc aag gcg 194
129 Asn Asp Val Cys Cys Lys Thr Cys Pro Ser Gly Thr Phe Val Lys Ala
130 50 55 60
132 ccc tgc aaa atc ccc cat act caa gga caa tgt gag aag tgt cac cca 242
133 Pro Cys Lys Ile Pro His Thr Gln Gly Gln Cys Glu Lys Cys His Pro
134 65 70 75
136 gga aca ttc aca ggg aaa gat aat ggc ctg cat gat tgt gaa ctt tgc 290

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137 Gly Thr Phe Thr Gly Lys Asp Asn Gly Leu His Asp Cys Glu Leu Cys
138          80          85          90
140 tcc acc tgt gat aaa gac cag aat atg gtg gct gac tgt tct gcc acc      338
141 Ser Thr Cys Asp Lys Asp Gln Asn Met Val Ala Asp Cys Ser Ala Thr
142          95          100          105
144 agt gac cgg aaa tgc gag tgc caa ata ggt ctt tac tac tat gac cca      386
145 Ser Asp Arg Lys Cys Glu Cys Gln Ile Gly Leu Tyr Tyr Tyr Asp Pro
146 110          115          120          125
148 aaa ttt ccg gaa tca tgc cgc cca tgt acc aag tgt ccc caa gga atc      434
149 Lys Phe Pro Glu Ser Cys Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile
150          130          135          140
152 cct gtc ctc cag gaa tgc aac tcc aca gct aac act gtg tgc agt tca      482
153 Pro Val Leu Gln Glu Cys Asn Ser Thr Ala Asn Thr Val Cys Ser Ser
154          145          150          155
156 tct gtt tca aat ccc aga aac tgg ctg ttc cta ctg atg cta att gtc      530
157 Ser Val Ser Asn Pro Arg Asn Trp Leu Phe Leu Leu Met Leu Ile Val
158          160          165          170
160 ttc tgt atc tgaagaagat aaagggttcta cagatgggtgt ctgtagcttc      579
161 Phe Cys Ile
162          175
164 cttttattgc tgtgaagaga aaccatggag gcaactcttt cattttattt tatttttttaa      639
166 tgtcttgaac ttgatttgaa gaccaggctg gactcaaact cacagagatc cggactaggc      699
168 acctctaata taggaaaaca ttgaattggg actggcttac agtttcagaa gttctgtcca      759
170 tgattatcat agtgcgaagc atggaggcac ggaggcacac atggtgctgg agaagaagct      819
172 gagagtctct catcttgatc tgcaagcaat aaaaggagac tgtgtgccac actacacata      879
174 gcttgaacat aggagacctc aaagcctgtc cccacagtga caaacttcct ccaacaagggt      939
176 catacctcct aataataacca tttcttatga ggcaagcatt caaacacatg agtctatgag      999
178 ggccaaacca attcaaacca ccacagggtta acaattgccc tctgcagctc tctggtggag      1059
180 gccctccttg agagtaagta acaatttaga tgaaggcaag tcctggtatc aggtccaaaa      1119
182 gaaactcagg atgaatggct cactgtgggt cctattaaca tactgaagaa catgacctca      1179
184 ccttagactt ctccacctca ctggcttccc ttcccctagc ttctcattcc caggtaaccc      1239
186 tgccattttt tggtaatgtg ccttcttggg tcttctctc ctttccccct ctcttctggg      1299
188 ccttatttct cttctctccc cactctccac cagccgcctc ttaaggcctg agtcagtctg      1359
190 caggccatgt ttaactctact actttctctc tgctctggac tcatccagat gtctctggct      1419
192 gagctctccc tcctatctac aataaaacct tccccctaac cagaaatgga acagttttgt      1479
194 cctcactttg tacatctggg gcctgaaacc      1509
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198 <211> LENGTH: 43
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: synthetically generated primer
205 <400> SEQUENCE: 4
206 gcggccgcga attctgacta actgacgggg gggggggggg ggg      43
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 26
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:

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215 <223> OTHER INFORMATION: synthetically generated primer
217 <400> SEQUENCE: 5
218 ccgcgagctc gatatcaagc ttgtac 26
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 29
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: synthetically generated primer
229 <400> SEQUENCE: 6
230 ggcgctcgag ctatagttcg aacatggag 29
233 <210> SEQ ID NO: 7
234 <211> LENGTH: 29
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: synthetically generated primer
241 <400> SEQUENCE: 7
242 gaggtacaag cttgatatcg agctcgagg 29
245 <210> SEQ ID NO: 8
246 <211> LENGTH: 23
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: synthetically generated primer
253 <400> SEQUENCE: 8
254 gccgcgaatt ctgactaact gac 23
257 <210> SEQ ID NO: 9
258 <211> LENGTH: 24
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: synthetically generated primer
265 <400> SEQUENCE: 9
266 ggatccttca actgtcccga tggc 24
269 <210> SEQ ID NO: 10
270 <211> LENGTH: 26
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: synthetically generated primer
277 <400> SEQUENCE: 10
278 gaattccaca cagtgttagc tgtgga 26
281 <210> SEQ ID NO: 11
282 <211> LENGTH: 36
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: synthetically generated primer

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294 <211> LENGTH: 35
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: synthetically generated primer
301 <400> SEQUENCE: 12
302 ccg gatcctc agatacagaa gacaattagc atcag 35
305 <210> SEQ ID NO: 13
306 <211> LENGTH: 123
307 <212> TYPE: PRT
308 <213> ORGANISM: Mus musculus
310 <400> SEQUENCE: 13
311 Cys Pro Gly Gly Lys Tyr Val His Ser Lys Asn Asn Ser Ile Cys Cys
312 1 5 10 15
314 Thr Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
315 20 25 30
317 Gly Arg Asp Thr Val Cys Arg Glu Cys Glu Lys Gly Thr Phe Thr Ala
318 35 40 45
320 Ser Gln Asn Tyr Leu Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys
321 50 55 60
323 Glu Met Ser Gln Val Glu Ile Ser Pro Cys Gln Ala Asp Lys Asp Thr
324 65 70 75 80
326 Val Cys Gly Cys Lys Glu Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr
327 85 90 95
329 His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr
330 100 105 110
332 Ile Pro Cys Lys Glu Thr Gln Asn Thr Val Cys
333 115 120
336 <210> SEQ ID NO: 14
337 <211> LENGTH: 118
338 <212> TYPE: PRT
339 <213> ORGANISM: Mus musculus
341 <400> SEQUENCE: 14
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343 1 5 10 15
345 Pro Ser Gly Thr Phe Val Lys Ala Pro Cys Lys Ile Pro His Thr Gln
346 20 25 30
348 Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Gly Lys Asp Asn
349 35 40 45
351 Gly Leu His Asp Cys Glu Leu Cys Ser Thr Cys Asp Lys Asp Gln Asn
352 50 55 60
354 Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Glu Cys Gln
355 65 70 75 80
357 Ile Gly Leu Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro
358 85 90 95
360 Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser

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VERIFICATION SUMMARY

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